Supplementary material

Figure S1 CLDN expression levels (mean value indicated by the horizontal bars) in normal colon mucosa (NM), primary tumors (PT) and hepatic metastases (HM). The Affymetrix RNA expression data were log2 transformed; *P*-values calculated with the Kruskal-Wallis test.

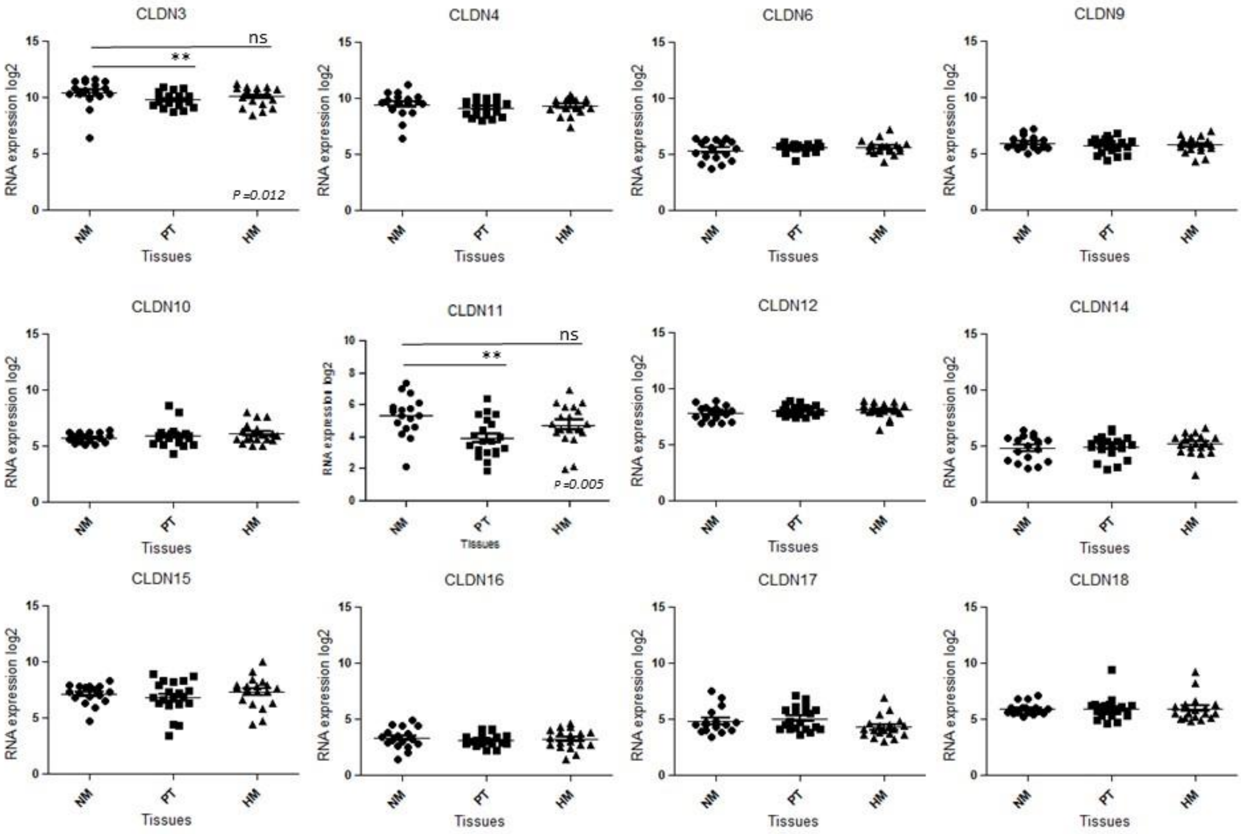

Figure S2 Mean CLDN expression in 15 paired primary CRC (PT) and normal mucosa (NM) samples.

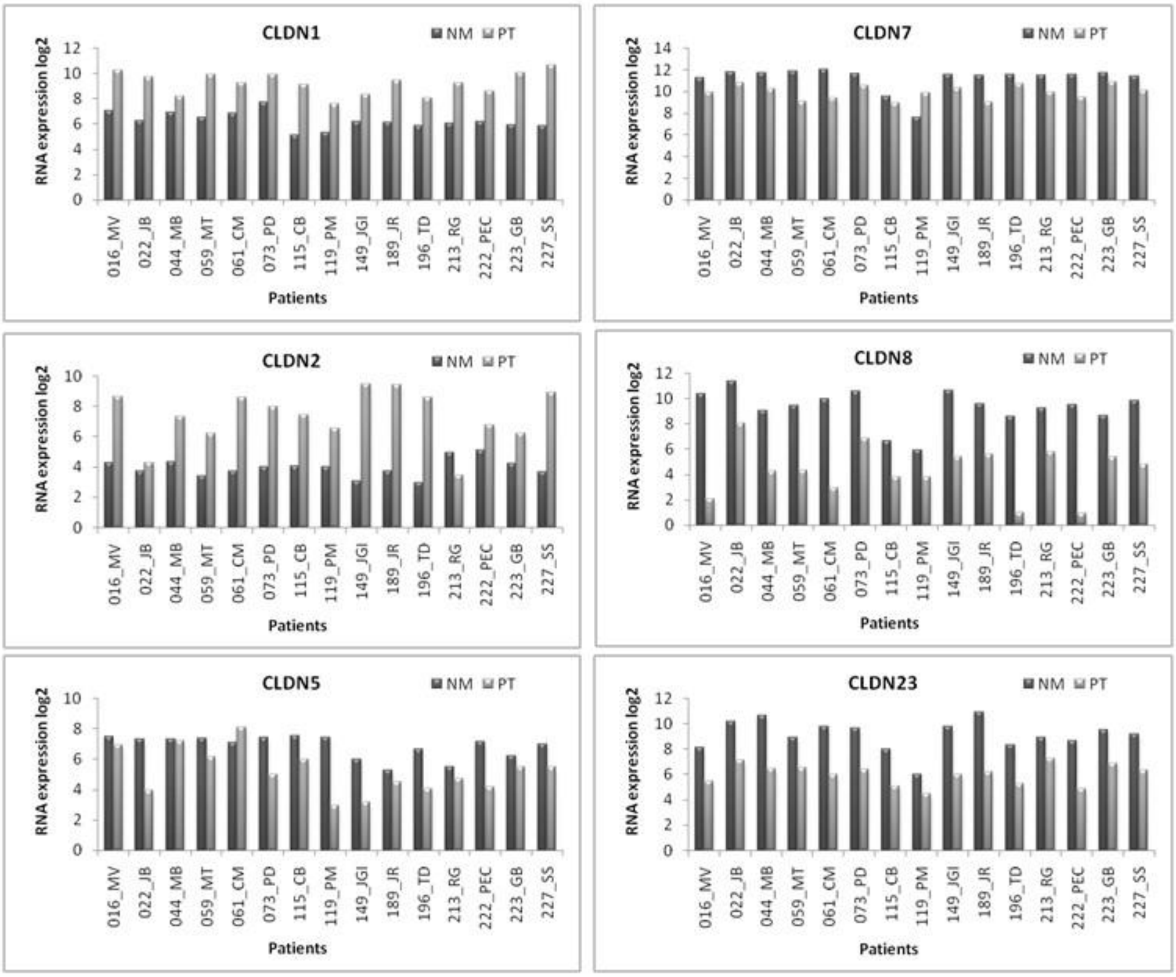

Figure S3 Differential CLDN gene expression in CRC samples classified according to the Marisa's classification (C1 to C6). (**A**) CLDN genes upregulated in tumors compared with normal mucosa. (**B**) CLDN genes downregulated in tumors compared with normal mucosa. (**C**) CLDN genes with similar expression in normal mucosa and tumors. The red horizontal line indicates CLDN expression in the normal mucosa within the CRC samples. The arrow highlights the subtype where CLDN expression is the most significantly different compared with the other subtypes. (Kruskal-Wallis/Dunn's test).

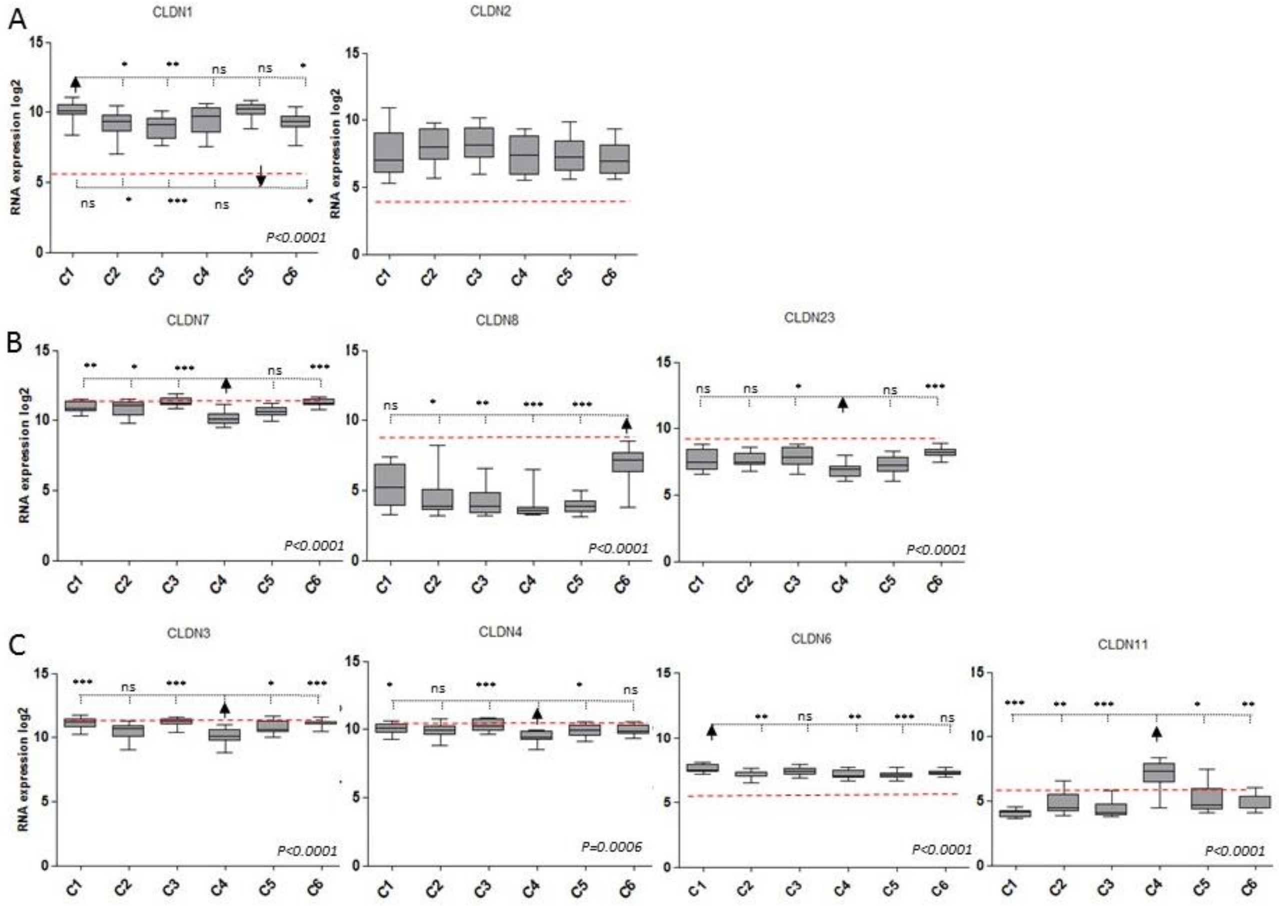

Figure S4 Association of CLDN2 or CLDN4 gene expression level (high/low relative to the median) and overall survival (OS) (log-rank test) (**A**) in 80 CRC samples from the Tsuji's cohort and (**B**) in the 143 CRC samples from the study cohort belonging to the indicated molecular subtypes (143 patients' cohort).

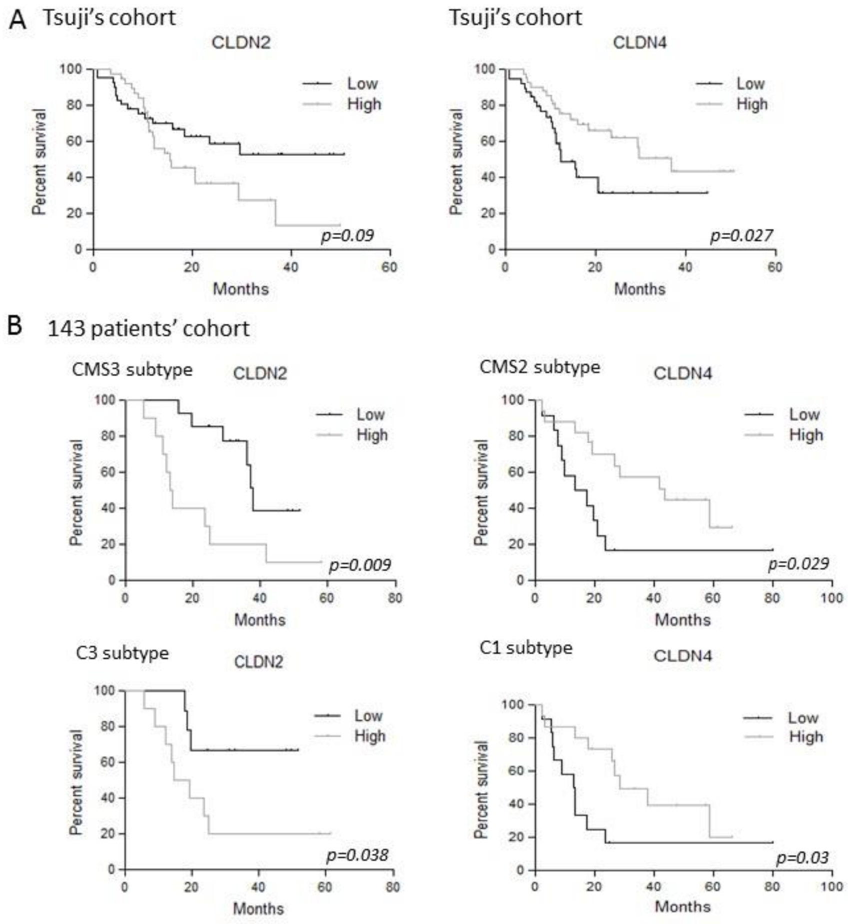

Figure S5 Association of CLDN gene expression level (high/low relative to the median) with progression-free survival (PFS) in the indicated CRC subtypes (log-rank test).